

Appl. No. : 09/853,257
Filed : May 10, 2001

REMARKS

Applicants have received the Office Action mailed September 13, 2002, stating that the above-captioned patent application fails to comply with the sequence rules because the sequences in Figure 1 are not listed in the sequence listing and are not identified by sequence identifier in the Brief Description of the Drawings.

Applicants request entry of the instant Amendment which replaces the paper copy of the existing sequence listing with a new paper copy of the sequence listing on substitute sheets as provided herewith. This amendment is supported by Figure 1 and thus the substitute sheets include no new matter. This amendment to the paper copy is accompanied by a substitute copy of the computer readable form including all previously submitted data with the amendment incorporated therein. This amendment is also supported by Figure 1 and thus the substitute copy of the computer readable form includes no new matter. Applicants also request entry of the instant Amendment to the Brief Description of the Drawings in which the sequences in Figure 1 are identified by sequence identifier.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

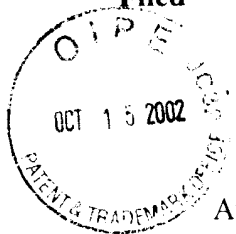
KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: October 9, 2002

By: Joseph J. Mallon
Joseph J. Mallon
Registration No. 39,287
Attorney of Record
Customer No. 20,995
(619) 235 8550

AMEND
S:\DOCS\JOM\JOM-3882.DOC
09/30/02

Appl. No. : 09/853,257
Filed : May 10, 2001



VERSION WITH MARKINGS TO SHOW CHANGES MADE

At page 6, lines 2-12, the first paragraph has been amended to add sequence identifiers as follows:

Figure 1 shows an alignment of LuxO with other σ^{54} dependent transcriptional activator proteins. Panel A shows an amino acid sequence comparisons between the central portion of LuxO (aa's 134-355) (SEQ ID NO:10), and five other transcriptional activator proteins that interact with σ^{54} . These proteins are: NtrC of *S. typhimurium* (aa's 141-362) (SEQ ID NO:11), NifA of *K. pneumoniae* (aa's 213-43) (SEQ ID NO:12), DctD of *R. leguminosarum* (aa's 146-367) (SEQ ID NO:13), HydG of *E. coli* (aa's 142-363) (SEQ ID NO:14), and FlbD of *C. crescentus* (aa's 121-342) (SEQ ID NO:15). Amino acids that match the consensus generated for the set of sequences are boxed in black. The glycine rich region that encodes the nucleotide binding domain characteristic of σ^{54} -interacting proteins is underlined. Panel B shows a comparison of a C-terminal region of LuxO (SEQ ID NO:16) to that of NtrC (SEQ ID NO:17), HydG (SEQ ID NO:18) and FlbD (SEQ ID NO:19). In the box are the putative HTH DNA binding domains for LuxO, HydG and FlbD. The extended box shows the known HTH DNA binding region for NtrC.